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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,535

DATE: 03/04/2002

TIME: 15:50:14

Input Set : A:\10448-142001.TXT

Output Set: N:\CRF3\03042002\J076535.raw

```

4 <110> APPLICANT: Kapeller-Libermann, Rosana
5   Carroll, Joseph M.
7 <120> TITLE OF INVENTION: 23565, A NOVEL HUMAN ZINC
8   CARBOXYPEPTIDASE FAMILY MEMBER AND USES THEREOF
11 <130> FILE REFERENCE: 10448-142001
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/076,535
C--> 13 <141> CURRENT FILING DATE: 2002-02-15
13 <150> PRIOR APPLICATION NUMBER: 60/269,440
14 <151> PRIOR FILING DATE: 2001-02-16
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1687
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (160)...(1467)
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: 10, 1685
31 <223> OTHER INFORMATION: n = A,T,C or G
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35 tctcaggccg ggctttccag cctctaggtg ctgtgctgtc ctgaggcctg ggccatgggtg      120
36 cccaaggaaa gccctgaag ctcaccagga ggaagaagc atg cag ggc act cct          174
37                                     Met Gln Gly Thr Pro
38                                     1           5
40 gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg acg ctc          222
41 Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg Thr Leu
42                                     10           15           20
44 ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg aat ttc          270
45 Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met Asn Phe
46                                     25           30           35
48 aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag cag ctt          318
49 Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys Gln Leu
50                                     40           45           50
52 tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg gac ttc          366
53 Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val Asp Phe
54                                     55           60           65
56 tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga gtt cct          414
57 Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg Val Pro
58 70                                     75           80           85
60 ttc tcc gaa ctg aaa gac atc aaa gct tat ctg gag tct cat gga ctt          462

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61	Phe	Ser	Glu	Leu	Lys	Asp	Ile	Lys	Ala	Tyr	Leu	Glu	Ser	His	Gly	Leu	
62				90					95						100		
64	gct	tac	agc	atc	atg	ata	aag	gac	atc	cag	gtg	ctg	ctg	gat	gag	gaa	510
65	Ala	Tyr	Ser	Ile	Met	Ile	Lys	Asp	Ile	Gln	Val	Leu	Leu	Asp	Glu	Glu	
66				105					110					115			
68	aga	cag	gcc	atg	gcg	aaa	tcc	cgc	cgg	ctg	gag	cgc	agc	acc	aac	agc	558
69	Arg	Gln	Ala	Met	Ala	Lys	Ser	Arg	Arg	Leu	Glu	Arg	Ser	Thr	Asn	Ser	
70				120				125						130			
72	ttc	agt	tac	tca	tca	tac	cac	acc	ctg	gag	gag	ata	tat	agc	tgg	att	606
73	Phe	Ser	Tyr	Ser	Ser	Tyr	His	Thr	Leu	Glu	Glu	Ile	Tyr	Ser	Trp	Ile	
74				135				140						145			
76	gac	aac	ttt	gta	atg	gag	cat	tcc	gat	att	gtc	tca	aaa	att	cag	att	654
77	Asp	Asn	Phe	Val	Met	Glu	His	Ser	Asp	Ile	Val	Ser	Lys	Ile	Gln	Ile	
78	150					155					160					165	
80	ggc	aac	agc	ttt	gaa	aac	cag	tcc	att	ctt	gtc	ctg	aag	ttc	agc	act	702
81	Gly	Asn	Ser	Phe	Glu	Asn	Gln	Ser	Ile	Leu	Val	Leu	Lys	Phe	Ser	Thr	
82					170					175					180		
84	gga	ggt	tct	cgg	cac	cca	gcc	atc	tgg	atc	gac	act	gga	att	cac	tcc	750
85	Gly	Gly	Ser	Arg	His	Pro	Ala	Ile	Trp	Ile	Asp	Thr	Gly	Ile	His	Ser	
86				185					190						195		
88	cgg	gag	tgg	atc	acc	cat	gcc	acc	ggc	atc	tgg	act	gcc	aat	aag	att	798
89	Arg	Glu	Trp	Ile	Thr	His	Ala	Thr	Gly	Ile	Trp	Thr	Ala	Asn	Lys	Ile	
90				200				205						210			
92	gtc	agt	gat	tat	ggc	aaa	gac	cgt	gtc	ctg	aca	gac	ata	ctg	aat	gcc	846
93	Val	Ser	Asp	Tyr	Gly	Lys	Asp	Arg	Val	Leu	Thr	Asp	Ile	Leu	Asn	Ala	
94				215				220					225				
96	atg	gac	atc	ttc	ata	gag	ctc	gtc	aca	aac	cct	gat	ggg	ttt	gct	ttt	894
97	Met	Asp	Ile	Phe	Ile	Glu	Leu	Val	Thr	Asn	Pro	Asp	Gly	Phe	Ala	Phe	
98	230					235					240				245		
100	acc	cac	agc	atg	aac	cgc	tta	tgg	cgg	aag	aac	aag	tcc	atc	aga	cct	942
101	Thr	His	Ser	Met	Asn	Arg	Leu	Trp	Arg	Lys	Asn	Lys	Ser	Ile	Arg	Pro	
102					250						255				260		
104	gga	atc	ttc	tgc	atc	ggc	gtg	gat	ctc	aac	agg	aac	tgg	aag	tcg	ggt	990
105	Gly	Ile	Phe	Cys	Ile	Gly	Val	Asp	Leu	Asn	Arg	Asn	Trp	Lys	Ser	Gly	
106				265					270						275		
108	ttt	gga	gga	aat	ggt	tct	aac	agc	aac	ccc	tgc	tca	gaa	act	tat	cac	1038
109	Phe	Gly	Gly	Asn	Gly	Ser	Asn	Ser	Asn	Pro	Cys	Ser	Glu	Thr	Tyr	His	
110				280				285						290			
112	ggg	ccc	tcc	cct	cag	tcg	gag	tcg	gag	gtg	gct	gcc	ata	gtg	aac	ttc	1086
113	Gly	Pro	Ser	Pro	Gln	Ser	Glu	Ser	Glu	Val	Ala	Ala	Ile	Val	Asn	Phe	
114				295			300					305					
116	atc	aca	gcc	cat	ggc	aac	ttc	aag	gct	ctg	atc	tcc	atc	cac	agc	tac	1134
117	Ile	Thr	Ala	His	Gly	Asn	Phe	Lys	Ala	Leu	Ile	Ser	Ile	His	Ser	Tyr	
118	310					315					320					325	
120	tct	cag	atg	ctt	atg	tac	cct	tac	ggc	cga	ttg	ctg	gag	ccc	gtt	tca	1182
121	Ser	Gln	Met	Leu	Met	Tyr	Pro	Tyr	Gly	Arg	Leu	Leu	Glu	Pro	Val	Ser	
122					330					335					340		
124	aat	cag	agg	gag	ttg	tac	gat	ctt	gcc	aag	gat	gcg	gtg	gag	gcc	ttg	1230
125	Asn	Gln	Arg	Glu	Leu	Tyr	Asp	Leu	Ala	Lys	Asp	Ala	Val	Glu	Ala	Leu	

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126          345          350          355
128 tat aag gtc cat ggg atc gag tac att ttt ggc agc atc agc acc acc      1278
129 Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly Ser Ile Ser Thr Thr
130          360          365          370
132 ctc tat gtg gcc agt ggg atc acc gtc gac tgg gcc tat gac agt ggc      1326
133 Leu Tyr Val Ala Ser Gly Ile Thr Val Asp Trp Ala Tyr Asp Ser Gly
134          375          380          385
136 atc aag tac gcc ttc agc ttt gag ctc cgg gac act ggg cag tat ggc      1374
137 Ile Lys Tyr Ala Phe Ser Phe Glu Leu Arg Asp Thr Gly Gln Tyr Gly
138 390          395          400          405
140 ttc ctg ctg ccg gcc aca cag atc atc ccc acg gcc cag gag acg tgg      1422
141 Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr Ala Gln Glu Thr Trp
142          410          415          420
144 atg gcg ctt cgg acc atc atg gag cac acc ctg aat cac ccc tac      1467
145 Met Ala Leu Arg Thr Ile Met Glu His Thr Leu Asn His Pro Tyr
146          425          430          435
148 tagcagcacg actgagggca ggaggctcca tccttctccc caaggtotgt ggctcctccc      1527
149 gaaacccaag ttatgcatcc ccatcccat gccctcatcc cgacctetta gaaaataaat      1587
150 acaagtttga acaggcaaaa aaaaaaaaaa aaaaaaaaaa tggcggccgc aagcttattc      1647
W--> 151 ctttaagtga gggttaattt tagcttggca ctggccgncg      1687
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 436
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 2
159 Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
160 1          5          10          15
161 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
162          20          25          30
163 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
164          35          40          45
165 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
166          50          55          60
167 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
168 65          70          75          80
169 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu
170          85          90          95
171 Glu Ser His Gly Leu Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val
172          100          105          110
173 Leu Leu Asp Glu Glu Arg Gln Ala Met Ala Lys Ser Arg Arg Leu Glu
174          115          120          125
175 Arg Ser Thr Asn Ser Phe Ser Tyr Ser Ser Tyr His Thr Leu Glu Glu
176          130          135          140
177 Ile Tyr Ser Trp Ile Asp Asn Phe Val Met Glu His Ser Asp Ile Val
178 145          150          155          160
179 Ser Lys Ile Gln Ile Gly Asn Ser Phe Glu Asn Gln Ser Ile Leu Val
180          165          170          175
181 Leu Lys Phe Ser Thr Gly Gly Ser Arg His Pro Ala Ile Trp Ile Asp
182          180          185          190

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183 Thr Gly Ile His Ser Arg Glu Trp Ile Thr His Ala Thr Gly Ile Trp
184      195      200      205
185 Thr Ala Asn Lys Ile Val Ser Asp Tyr Gly Lys Asp Arg Val Leu Thr
186      210      215      220
187 Asp Ile Leu Asn Ala Met Asp Ile Phe Ile Glu Leu Val Thr Asn Pro
188 225      230      235      240
189 Asp Gly Phe Ala Phe Thr His Ser Met Asn Arg Leu Trp Arg Lys Asn
190      245      250      255
191 Lys Ser Ile Arg Pro Gly Ile Phe Cys Ile Gly Val Asp Leu Asn Arg
192      260      265      270
193 Asn Trp Lys Ser Gly Phe Gly Gly Asn Gly Ser Asn Ser Asn Pro Cys
194      275      280      285
195 Ser Glu Thr Tyr His Gly Pro Ser Pro Gln Ser Glu Ser Glu Val Ala
196      290      295      300
197 Ala Ile Val Asn Phe Ile Thr Ala His Gly Asn Phe Lys Ala Leu Ile
198 305      310      315      320
199 Ser Ile His Ser Tyr Ser Gln Met Leu Met Tyr Pro Tyr Gly Arg Leu
200      325      330      335
201 Leu Glu Pro Val Ser Asn Gln Arg Glu Leu Tyr Asp Leu Ala Lys Asp
202      340      345      350
203 Ala Val Glu Ala Leu Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly
204      355      360      365
205 Ser Ile Ser Thr Thr Leu Tyr Val Ala Ser Gly Ile Thr Val Asp Trp
206      370      375      380
207 Ala Tyr Asp Ser Gly Ile Lys Tyr Ala Phe Ser Phe Glu Leu Arg Asp
208 385      390      395      400
209 Thr Gly Gln Tyr Gly Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr
210      405      410      415
211 Ala Gln Glu Thr Trp Met Ala Leu Arg Thr Ile Met Glu His Thr Leu
212      420      425      430
213 Asn His Pro Tyr
214      435
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 1311
218 <212> TYPE: DNA
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 3
222 atgcagggca ctcttgagg cgggacgcgc cctgggccaat cccccgtgga caggcggacg      60
223 ctctctggtct tcagctttat cctggcagca gctttggggcc aaatgaattt cacaggggac      120
224 caggttcttc gagtcctggc caaagatgag aagcagcttt cacttctcgg ggaatctggag      180
225 ggcttgaaac ccagaagggt ggacttctgg cgtggcccag ccaggcccag cctccctgtg      240
226 gatatgagag ttcttttctc cgaactgaaa gacatcaaag cttatctgga gtctcatgga      300
227 ctggtttaca gcatcatgat aaaggacatc caggtgctgc tggatgagga aagacaggcc      360
228 atggcgaaat cccgccggct ggagcgcagc accaacagct tcagttactc atcataccac      420
229 accctggagg agatatatag ctggattgac aactttgtaa tggagcattc cgatattgtc      480
230 tcaaaaattc agattggcaa cagctttgaa aaccagtcca ttcttgctct gaagttcagc      540
231 actggagggt ctcggcaccc agccatctgg atcgacactg gaattcactc ccgggagtg      600
232 atcacccatg ccaccggcat ctggactgcc aataagattg tcagtgatta tggcaaagac      660
233 cgtgtcctga cagacatact gaatgccatg gacatcttca tagagctcgt cacaaacct      720

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234 gatggggttg cttttaccca cagcatgaac cgcttatggc ggaagaacaa gtccatcaga      780
235 cctggaatct tctgcatcgg cgtggatctc aacaggaaact ggaagtcggg ttttggagga      840
236 aatgggttcta acagcaaccc ctgctcagaa acttatcacg ggccctcccc tcagtcggag      900
237 tcggaggttg ctgccatagt gaacttcacg acagcccatg gcaacttcaa ggctctgatc      960
238 tccatccaca gctactctca gatgcttatg tacccttacg gccgattgct ggagcccgtt     1020
239 tcaaatacaga gggagttgta cgatcttgcc aaggatgcgg tggaggcctt gtataaggtc     1080
240 catgggatcg agtacatttt tggcagcatc agcaccaccc tctatgtggc cagtgggatc     1140
241 accgtcgact gggcctatga cagtggcatc aagtagcctt tcagctttga gctccgggac     1200
242 actgggcagt atggcttcct gctgccggcc acacagatca tccccacggc ccaggagacg     1260
243 tggatggcgc ttcggaccat catggagcac accctgaatc acccctacta g              1311
245 <210> SEQ ID NO: 4
246 <211> LENGTH: 304
247 <212> TYPE: PRT
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Consensus sequence
253 <400> SEQUENCE: 4
254 Tyr His Asn Leu Glu Glu Ile Tyr Ala Trp Leu Asp Leu Leu Val Ser
255 1 5 10 15
256 Asn Phe Pro Asp Leu Val Ser Lys Val Ser Ile Gly Lys Ser Tyr Glu
257 20 25 30
258 Gly Arg Asp Leu Lys Val Leu Lys Ile Ser Asp Asn Pro Ala Thr Gly
259 35 40 45
260 Glu Asn Glu Pro Glu Val Phe Ala Val Ala Gly Trp Ile His Ala Arg
261 50 55 60
262 Glu Trp Val Thr Ser Ala Thr Leu Leu Trp Leu Lys Glu Leu Val
263 65 70 75 80
264 Ala Asn Tyr Gly Ser Asp Lys Thr Ile Thr Lys Leu Leu Asp Gly Leu
265 85 90 95
266 Asp Leu Phe Tyr Ile Leu Pro Val Phe Asn Pro Asp Gly Tyr Ala Tyr
267 100 105 110
268 Ser Ile Thr Thr Asp Ser Tyr Arg Met Trp Arg Lys Thr Arg Ser Pro
269 115 120 125
270 Asn Ala Gly Ser Phe Cys Val Gly Thr Asp Pro Asn Arg Asn Trp Tyr
271 130 135 140
272 Ala Gln Trp Gly Gly Met Gly Ala Ser Ser Tyr Ser Pro Cys Ser Glu
273 145 150 155 160
274 Thr Tyr Glu Gly Thr Ala Pro Phe Ser Glu Pro Glu Thr Lys Ala Val
275 165 170 175
276 Glu Asp Phe Ile Arg Ser Trp Leu Gly Gly Lys Gln Asn Ile Lys
277 180 185 190
278 Ala Tyr Ile Thr Phe His Ser Tyr Ser Gln Leu Leu Leu Tyr Pro Tyr
279 195 200 205
280 Gly Tyr Asp Tyr Asn Leu Asn Pro Asp Ala Asn Asp Leu Asp Glu Leu
281 210 215 220
282 Ser Asp Leu Lys Ile Ala Ala Asp Ala Leu Ser Ala Arg His Gly Thr
283 225 230 235 240
284 Tyr Tyr Thr Leu Gly Leu Pro Gly Ser Ser Thr Ile Tyr Pro Ala Ser
285 245 250 255

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/076,535

DATE: 03/04/2002

TIME: 15:50:15

Input Set : A:\10448-142001.TXT

Output Set: N:\CRF3\03042002\J076535.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1